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OM protein - protein search, using sw model

Run on:

August 24, 2005, 18:40:12 ; Search time 161 Seconds

(without alignments)

248.086 Million cell updates/sec

Title: US-09-763-393-1
Perfect score: 541
Sequence: 1 MSARVRSRSGRGDGQEAQD.....EKTPPNPKHAKTKEAGDGQP 102

Scoring table: BioSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AR,*

Listed first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1
US-10-205-823-186
; Sequence 186, Application US/10205823

; Publication No. US20030108963A1

; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert

; APPLICANT: Monahan, John E.

; APPLICANT: Endege, Wilson O.

; APPLICANT: Gannavarapu, Manjula

; APPLICANT: Gorbaucheva, Belia

; APPLICANT: Hoersch, Sebastian

; APPLICANT: Kamatkar, Shubhangi

; APPLICANT: Wonsey, Angela M.

; APPLICANT: Glatt, Karen

; APPLICANT: Zhao, Xumei

; APPLICANT: Anderson, Dustin

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

; FILE REFERENCE: MEI-044

; CURRENT APPLICATION NUMBER: US/10/205,823

; CURRENT FILING DATE: 2002-07-25

; PRIORITY APPLICATION NUMBER: 60/307,982

; PRIORITY FILING DATE: 2001-07-25

; PRIORITY APPLICATION NUMBER: 60/314,356

; PRIORITY FILING DATE: 2001-08-22

; PRIORITY APPLICATION NUMBER: 60/325,020

; PRIORITY APPLICATION NUMBER: 60/325,020

; PRIORITY FILING DATE: 2001-09-25

; PRIORITY APPLICATION NUMBER: 60/341,746

1	541	100.0	102	14	US-10-205-823-186	Sequence 186, App	Sequence 38, Appl
2	541	100.0	102	16	US-10-801-273-2	Sequence 2, App	Sequence 28, Appl
3	528	97.6	99	14	US-10-131-405-46	Sequence 46, App	Sequence 37, Appl
4	528	97.6	99	15	US-10-139-854-46	Sequence 46, App	Sequence 4, Appl
5	528	97.6	99	15	US-10-150-813-46	Sequence 46, App	Sequence 37, Appl
6	528	97.6	99	15	US-10-150-811-46	Sequence 46, App	Sequence 37, Appl
7	295.5	54.6	109	14	US-10-131-409-28	Sequence 28, App	Sequence 4, Appl
8	295.5	54.6	109	14	US-10-131-409-38	Sequence 38, App	Sequence 37, Appl
9	295.5	54.6	109	15	US-10-139-854-28	Sequence 28, App	Sequence 37, Appl
10	295.5	54.6	109	15	US-10-139-854-38	Sequence 28, App	Sequence 37, Appl
11	295.5	54.6	109	15	US-10-150-813-28	Sequence 28, App	Sequence 37, Appl

SEQ ID NO: 186 LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-205-823-186

Query Match 100.0%; Score 541; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.1e-42; Mismatches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Seq ID NO: 2

Qy 1 MSARRRSRGGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 60
Db 1 MSARVRSRSGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 60

Qy 61 GDCQEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 102
Db 61 GDCQEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 102

RESULT 2
US-10-821-273-2
; Sequence(2) Application US/10821273 ✓
; Publication No. US20040248256A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Metberg, David
; APPLICANT: Tracy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: DiBiasio-Smith, Elizabeth
; APPLICANT: Widow, Angela
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000101. CURRENT APPLICATION NUMBER: US/10/821,273
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 09/306,111
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 60/084,564 ✓
; PRIOR FILING DATE: 1998-05-31
; PRIOR APPLICATION NUMBER: US 60/087,645
; PRIOR FILING DATE: 1998-05-02
; PRIOR APPLICATION NUMBER: US 60/093,712 ✓
; PRIOR FILING DATE: 1998-02-22
; PRIOR APPLICATION NUMBER: US 60/094,935
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 60/095,880
; PRIOR FILING DATE: 1998-02-10
; PRIOR APPLICATION NUMBER: US 60/096,068
; PRIOR FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 2

Qy 1 MSARRRSRGGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 60
Db 1 MSARVRSRSGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 60

Qy 61 GDCQEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 102
Db 61 GDCQEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 102

RESULT 3
US-10-131-409-46
; Sequence 46, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Malvankar et al.
; TITLE OF INVENTION: No. US20030199465A1 Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 15966-675CIP/CON1 CURRENT APPLICATION NUMBER: US/10/131,409 PRIOR FILING DATE: 2002-10-24 PRIOR APPLICATION NUMBER: 09/898,954 PRIOR FILING DATE: 2001-07-03 PRIOR APPLICATION NUMBER: 60/182,733 PRIOR FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 60/182,724 PRIOR FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 60/183,896 PRIOR FILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: 60/184,497 PRIOR FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: 60/224,157 PRIOR FILING DATE: 2000-08-10 PRIOR APPLICATION NUMBER: 60/184,482 PRIOR FILING DATE: 2000-02-23 PRIOR APPLICATION NUMBER: 60/184,744 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: 60/197,083 PRIOR FILING DATE: 2000-04-13 PRIOR APPLICATION NUMBER: 60/233,405 PRIOR FILING DATE: 2000-09-18 Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 135 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO: 46 LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-131-409-46 ✓
Query Match 97.6%; Score 528; DB 14; Length 99; Best Local Similarity 100.0%; Pred. No. 3.3e-41; Mismatches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Seq ID NO: 2

Qy 4 RVRSRSRGGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 63
Db 1 RVRSRSRGGRGQEAAPDVAFPGESQEEPTNDQIEPQEREGTPPIRKVE 60

Qy 64 QEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 102
Db 61 QEMDLEKTRSERGDGSVKEKTPNPKHAKTKHAGDGP 99

RESULT 4
US-10-139-854-46
; Sequence 46, Application US/10139854
; Publication No. US2003022971A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 15966-675C0N2 CURRENT APPLICATION NUMBER: US/10/139,854 PRIOR APPLICATION NUMBER: 09/783,429 PRIOR FILING DATE: 2001-02-14 PRIOR APPLICATION NUMBER: 60/182,733 PRIOR FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 60/182,724 PRIOR FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 60/183,896 PRIOR FILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: 60/184,497

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; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-854-46

; Query Match 97.6%; Score 528; DB 15; Length 99;
; Best Local Similarity 100.0%; Pred. No. 3.3e-41; Mismatches 0; Indels 0; Gaps 0;
; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-854-46

RESULT 5
US-10-150-813-46
; Sequence 46, Application US/10150813
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Majumdar et al.
; TITLE OF INVENTION: No. US20040010120A1 Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675C1P2C0N1
; CURRENT APPLICATION NUMBER: US/10/150,811
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970,607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-150-811-46

RESULT 6
US-10-150-811-46
; Sequence 46, Application US/10150813
; Publication No. US20040010120A1
; GENERAL INFORMATION:
; APPLICANT: Majumdar et al.
; TITLE OF INVENTION: No. US20040010120A1 Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675C1P2C0N1
; CURRENT APPLICATION NUMBER: US/10/150,811
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 09/970,607
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/224,157
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-150-811-46

RESULT 7
US-10-131-409-28
; Sequence 28, Application US/10131409
; Publication No. US20030199465A1
; GENERAL INFORMATION:
; APPLICANT: Majumdar et al.
; TITLE OF INVENTION: No. US20030199465A1 Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675C1P2C0N1
; CURRENT APPLICATION NUMBER: US/10/131,409

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CURRENT FILING DATE: 2002-10-24 ;

PRIOR APPLICATION NUMBER: 09/898,954 ;

PRIOR FILING DATE: 2001-07-03 ;

PRIOR APPLICATION NUMBER: 60/182,733 ;

PRIOR FILING DATE: 2000-02-15 ;

PRIOR APPLICATION NUMBER: 60/182,724 ;

PRIOR FILING DATE: 2000-02-15 ;

PRIOR APPLICATION NUMBER: 60/183,896 ;

PRIOR FILING DATE: 2000-02-22 ;

PRIOR APPLICATION NUMBER: 60/184,497 ;

PRIOR FILING DATE: 2000-02-23 ;

PRIOR APPLICATION NUMBER: 60/182,157 ;

PRIOR FILING DATE: 2000-08-10 ;

PRIOR APPLICATION NUMBER: 60/184,482 ;

PRIOR FILING DATE: 2000-02-23 ;

PRIOR APPLICATION NUMBER: 60/184,744 ;

PRIOR FILING DATE: 2000-02-24 ;

PRIOR APPLICATION NUMBER: 60/197,083 ;

PRIOR FILING DATE: 2000-04-13 ;

PRIOR APPLICATION NUMBER: 60/233,405 ;

PRIOR FILING DATE: 2000-09-18 ;

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 135 ;

SOFTWARE: Patentin Ver. 2.1 ;

SEQ ID NO: 38 ;

LENGTH: 109 ;

TYPE: PRT ;

ORGANISM: Homo sapiens ;

US-10-131-409-28

Query Match 54.6%; Score 295.5; DB 14; Length 109;

Best Local Similarity 61.5%; Pred. No. 1e-19;

Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;

Qy 4 RVRSRSGRGQEAQDPDVAVAPGR-----SQQEPPTNDQDIEPGQREGTPPIERK 58

Db 6 RARSOSERGRNDOESSQPVGSVIVQEPTEEKRQQEPPTNDQDIEPGQREGTPPIERK 65

Qy 59 VEGDCQEMDLKTRSRGDSQDVKPDKTIPPKHAKTEAGDQP 102

Db 66 VEGDCQEMALLKIEDBFGDPDVREGIMPTFDLTKVLEAGDAQP 109

RESULT 8

US-10-131-409-38

Sequence 28, Application US/10139854

Publication No. US20030202971A1

GENERAL INFORMATION:

APPLICANT: Majumder, Kumud

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

CURRENT APPLICATION NUMBER: US/10/139,854

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 09/783,429

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/182,724

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/183,896

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/184,482

PRIOR FILING DATE: 2000-04-13

PRIOR APPLICATION NUMBER: 60/233,405

PRIOR FILING DATE: 2000-09-18

Remaining Prior Application data removed - See File Wrapper or PALM.

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 135 ;

SOFTWARE: Patentin Ver. 2.1 ;

SEQ ID NO: 38 ;

LENGTH: 109 ;

TYPE: PRT ;

ORGANISM: Homo sapiens ;

US-10-131-409-38

Query Match 54.6%; Score 295.5; DB 15; Length 109;

Best Local Similarity 61.5%; Pred. No. 1e-19;

Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;

Qy 4 RVRSRSGRGQEAQDPDVAVAPGR-----SQQEPPTNDQDIEPGQREGTPPIERK 58

Db 6 RARSOSERGRNDOESSQPVGSVIVQEPTEEKRQQEPPTNDQDIEPGQREGTPPIERK 65

Qy 59 VEGDCQEMDLKTRSRGDSQDVKPDKTIPPKHAKTEAGDQP 102

Db 66 VEGDCQEMALLKIEDBFGDPDVREGIMPTFDLTKVLEAGDAQP 109

RESULT 9

US-10-139-854-28

Sequence 28, Application US/10139854

Publication No. US20030202971A1

GENERAL INFORMATION:

APPLICANT: Majumder, Kumud

TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same

CURRENT APPLICATION NUMBER: US/10/139,854

CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 09/783,429

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 60/182,733

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 60/183,896

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: 60/184,497

PRIOR FILING DATE: 2000-02-23

PRIOR APPLICATION NUMBER: 60/233,405

PRIOR FILING DATE: 2000-09-18

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 126 ;

SOFTWARE: Patentin Ver. 2.1 ;

SEQ ID NO: 28 ;

LENGTH: 109 ;

TYPE: PRT ;

ORGANISM: Homo sapiens ;

US-10-139-854-28

Query Match 54.6%; Score 295.5; DB 15; Length 109;

Best Local Similarity 61.5%; Pred. No. 1e-19;

Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;

Qy 4 RVRSRSGRGQEAQDPDVAVAPGR-----SQQEPPTNDQDIEPGQREGTPPIERK 58

Db 6 RARSOSERGRNDOESSQPVGSVIVQEPTEEKRQQEPPTNDQDIEPGQREGTPPIERK 65

Qy 59 VEGDCQEMDLKTRSRGDSQDVKPDKTIPPKHAKTEAGDQP 102

Db 66 VEGDCQEMALLKIEDBFGDPDVREGIMPTFDLTKVLEAGDAQP 109

RESULT 10 ;
US-10-139-854-38 ;
; Sequence 38, Application US/10139854
; Publication No. US20030202971A1
; GENERAL INFORMATION:
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CICON2
; CURRENT APPLICATION NUMBER: US/10/139,854
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 09/783,429
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 28
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 38
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-139-854-38
Query Match Best Local Similarity 54.6%; Score 295.5; DB 15; Length 109;
Matches 64; Conservative 61.5%; Pred. No. 1e-19; Indels 5; Gaps 1;
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Qy 4 RVRSSRGGRGSGEAPDVAVFARGE----SQQEERTPDNQDIEQCRGSRGTPPIERK 58
Db 6 RARSQSERGRGNDQESQSPVSVIIVQEPTEEKQEQEPPTDNQDIEQCRGSRGTPPIERK 65
;
Qy 59 VEGDCQENDLEKTRSERGDGSVKEKTPPNPKHAKTVEAGDGQP 102
Db 66 VEGDCQENDLEKTRSERGDGSVKEKTPPNPKHAKTVEAGDGQP 109
;
RESULT 11 ;
US-10-150-813-28 ;
; Sequence 28, Application US/10150813
; Publication No. US2003022437A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-675CICON2
; CURRENT APPLICATION NUMBER: US/10/150,813
; PRIOR FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 09/898,954
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/182,733
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/182,724
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 60/183,896
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/184,497
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,482
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,744
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/197,083
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/233,405
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 38
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-150-813-28
Query Match Best Local Similarity 54.6%; Score 295.5; DB 15; Length 109;

Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;
 Qy 4 RVRSRSGRGDQEARPDVVAFVAGE---SQQEPTDNDIQCERGCTPIERK 58
 Db 6 RARSQSSERNGDQESSOPVGSVIVQEPTBEEKRQOERPTDNDIQCERGCTPIERK 65
 Qy 59 VEGDCQEMDLIEKTRSERGDGSDVKEKTPPNPKHAKTKERAGDGQP 102
 Db 66 VEGDCQEMALLKIEDBPGDPDVREGIMPTFDLTKVLEAGDAQP 109

RESULT 13
 US-10-150-811-28
 ; Sequence 28, Application US/10150811
 ; Publication No. US20040010120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malayankar et al.
 ; TITLE OF INVENTION: No. US20040010120A1 Polypeptides and Nucleic Acids Encoding Sam
 ; FILE REFERENCE: 15966-675C1P2CON1
 ; CURRENT APPLICATION NUMBER: US/10/150, 811
 ; PRIOR APPLICATION NUMBER: 03/970, 607
 ; PRIOR FILING DATE: 2001-10-03
 ; PRIOR APPLICATION NUMBER: 60/182, 733
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/182, 724
 ; PRIOR FILING DATE: 2000-02-15
 ; PRIOR APPLICATION NUMBER: 60/183, 896
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 60/184, 497
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/184, 157
 ; PRIOR FILING DATE: 2000-08-10
 ; PRIOR APPLICATION NUMBER: 60/184, 482
 ; PRIOR FILING DATE: 2000-02-23
 ; PRIOR APPLICATION NUMBER: 60/184, 744
 ; PRIOR FILING DATE: 2000-09-18
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 138
 ; SEQ ID NO 38
 ; LENGTH: 109
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-150-811-38
 ; Query Match 54.6%; Score 295.5; DB 15; Length 109;
 ; Best Local Similarity 61.5%; Pred. No. 1e-19; Mismatches 31; Indels 5; Gaps 1;
 ; Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;
 Qy 4 RVRSRSGRGDQEARPDVVAFVAGE---SQQEPTDNDIQCERGCTPIERK 58
 Db 6 RARSQSSERNGDQESSOPVGSVIVQEPTBEEKRQOERPTDNDIQCERGCTPIERK 65
 Qy 59 VEGDCQEMDLIEKTRSERGDGSDVKEKTPPNPKHAKTKERAGDGQP 102
 Db 66 VEGDCQEMALLKIEDBPGDPDVREGIMPTFDLTKVLEAGDAQP 109

RESULT 15
 US-10-029-386-21312
 ; Sequence 31312, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
 ; FILE REFERENCE: AEMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029, 386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Autamax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 31312
 ; LENGTH: 41
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AF238380.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.94
 ; OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.3
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
 ; OTHER INFORMATION: SWISSPROT HIT: 060829, EVALUE 1.00e-18
 ; US-10-029-386-31312
 ; Query Match 40.5%; Score 219; DB 14; Length 41;
 ; Best Local Similarity 100.0%; Pred. No. 4e-13; Mismatches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 US-10-150-811-38
 ; Sequence 38, Application US/10150811
 ; Publication No. US20040010120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Malayankar et al.
 ; TITLE OF INVENTION: No. US. 20040010120A1 Polypeptides and Nucleic Acids Encoding Sam
 ; FILE REFERENCE: 15966-675C1P2CON1
 ; CURRENT APPLICATION NUMBER: US/10/150, 811
 ; CURRENT FILING DATE: 2002-05-17

Thu Aug 25 08:49:42 2005

usb-09-763-393-1.rapb

Page 7

QY 57 RKVEGDCQENDLEKTRSERGDGSVKEKTPPNPKHAKTKEA 97
Db 1 RKVEGDCQENDLEKTRSERGDGSVKEKTPPNPKHAKTKEA 41

Search completed: August 24, 2005, 18:46:36
Job time : 169 secs

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GenCore version 5.1.6
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On protein - protein search, using sw model

Run on: August 24, 2005, 18:30:13 ; Search time 58 Seconds

(without alignments)
900.553 Million cell updates/sec

Title: US-09-763-393-1
Perfect score: 541
Sequence: 1 MSARYVRSRSGRGDGQEAPD..... EKTPPNPKHAKTKEAGDGQP 102

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03;*

- 1: uniprot_sprot;*
- 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	541	100.0	102	1	GGC1_HUMAN
2	176	32.5	130	2	Q96GII1
3	168.5	31.1	111	2	Q72ZK7
4	163.5	30.2	108	1	GGDS_HUMAN
5	156	28.8	111	1	GDD4_HUMAN
6	133	24.6	145	1	GGB1_HUMAN
7	131.5	24.3	111	1	GGD5_HUMAN
8	131	24.2	117	2	Q6NT33
9	127	23.5	116	1	GGB4_HUMAN
10	123	22.7	117	1	GGE5_HUMAN
11	123	22.7	117	1	GGE5_HUMAN
12	123	22.7	118	1	GGE3_HUMAN
13	122	22.6	117	1	GGB6_HUMAN
14	120	22.2	116	1	GGB2_HUMAN
15	120	22.2	116	2	Q6NT46
16	117	21.6	138	1	GGE1_HUMAN
17	116	21.4	117	1	GGE7_HUMAN
18	113	20.9	139	2	Q8YX5
19	112	20.7	829	2	QBNM60
20	112	20.7	861	2	Q95040
21	112	20.7	861	2	Q8TBY5
22	112	20.7	861	2	Q96J94
23	108.5	20.1	485	2	Q6NXX0
24	108.5	20.1	862	2	Q9JMB7
25	104.5	19.3	792	2	Q9KFO3
26	102.5	18.9	69	2	Q8WWM0
27	96.5	17.8	229	1	VR6425
28	96.5	17.8	325	2	Q44016
29	96.5	17.8	506	2	Q6ZP73
30	94.5	17.5	524	1	T2EA_XENLA
31	94.5	17.5	Q8JG17		Q8JG17_xenopus_lae

ALIGNMENTS

RESULT 1	ID	GGC1_HUMAN	STANDARD;	PRT;	102 AA.
	AC	Q008Z9;			16-OCT-2001 (Rel. 40, Created)
	DT				16-OCT-2001 (Rel. 40, Last sequence update)
	DT				05-JUL-2004 (Rel. 44, Lab annotation update)
	DE				G antigen family C 1 protein (Prostate-associated gene protein 4)
	DB				(PAGE-4) (PAGE-1) (JM27) (GAGE-9).
	GN				Name=GAGEC1; Synonyms=PAGE34;
	OS				Homo sapiens (Human)
	OC				Rukarvota; Metacoe; Chordata; Craniata; Vertebrata; Euteleostomi;
	OC				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	RN				NCBI_TaxID=9606;
	RP				SEQUENCE FROM N.A.
	RP				RX MEDLINE=9839318; PubMed=9724777; DOI=10.1073/pnas.95.18.10257;
	RA				Brinkmann U., Vasmatsu G., Lee B., Yerushalmi N., Essand M.,
	RA				Pastan I.; Nyakatura G., Hellebrand H., Drescher B., Rosenthal A.,
	RT				"PAGE-1, an X chromosome-linked GAGE-like gene that is expressed in normal and neoplastic prostate, testis, and uterus";
	RT				Proc. Natl. Acad. Sci. U.S.A. 95:10757-10762 (1998).
	RL				[2]
	RN				SEQUENCE FROM N.A.
	RC				TISSUE=Placenta.
	RC				RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
	RA				Strauberg R.L., Feingold B.E., Grouse L.H., Derge J.G., Meindl A.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
	RA				[3]
	RN				SEQUENCE FROM N.A.
	RC				DIATCHENKO L., Marusina K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshikuni S., Cernicci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McBryan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia K.M., Gay L.J., Hulyk S.W., Villano D.K., Munzy D.M., Sodergran B.J., Lu X., Gibbs R.A., RA Fabeij J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young R.C., Shvchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., RA Schnech A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
	CC				-- FUNCTION: Unknown.
	CC				-- TISSUE SPECIFICITY: Preferentially expressed in normal male and female reproductive tissues, prostate, fallopian tube,

CC. uterus, and placenta, as well as in prostate cancer, testicular cancer, and uterine cancer.
 CC. RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC. RN [2]
 CC. RP SEQUENCE FROM N.A.
 CC. RC TISSUE=Skin;
 CC. RA Straubberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC. RN [3]
 CC. RA Zendman A.J.W., van Kraats A.A., Weidle U.H., Ruiter D.J., Van Muilen G.N.P.; Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC. RN [4]
 CC. RA EMBL; BC009230; AAH09230.2;
 DR EMBL; AJ34352; CAC07642.1;
 DR InterPro; IPR008625; GAGE.
 DR EMBL; BC010897; AAH10897.1; -;
 DR Genew; HGNC:4108; GAGEQ1.
 DR H-InvDB; HIX016804; -;
 DR MIM; 300287; -;
 DR InterPro; IPR008625; GAGE.
 DR Pfam; PF05831; GAGE; 1.
 KW Multigene family;
 SQ SEQUENCE 102 AA; 11153 MW; C65D07AFBF73301B CRC64;
 Query Match 100.0%; Score 541; DB 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1. 6e-36;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MSARVRSRSRGADGVAVVAPGSESQOBEPPTNDQIDPQGQEREGTPPIERKVE 60
 Db 1 MSARVRSRSRGADGVAVVAPGSESQOBEPPTNDQIDPQGQEREGTPPIERKVE 60
 Query Match 32.5%; Score 176; DB 2; Length 130;
 Best Local Similarity 43.1%; Pred. No. 6. 3e-07;
 Matches 47; Conservative 11; Mismatches 43; Indels 8; Gaps 3;
 OY 1 MSARVRSRSRGADGVAVVAPGSESQOBEPPTNDQIDPQGQEREGTPPIERKVE 60
 Db 21 MSEHVTRSQSERGNDQESQSPGVPUVQOPTERQEREPPTNDQIGLPSGEKGEGAP 80
 Query Match 53 PIERKEGGCQEMDLEKTRSERGQSDVKEKTPNPKHAKTEAGDGQ 101
 Db 81 AVQGDWEAFOOBALKIEDAPGDPDVREGTLPFDPTKVLEAGEGQ 129
 RESULT 2
 O96GUL PRELIMINARY; PRT; 130 AA.
 ID O96GUL; Q8WNL9;
 AC O96GUL; Q8WNL9;
 DT 01-MAR-2004 (TREMBlrel. 25, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DT PAGE-5 protein.
 Name=PAGE-5;
 GN Homo sapiens (Human).
 OS Bukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo.
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhattacharyya N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetzen T.E.,
 RA Brownstein M.J., Uridin T.B., Toshiyuki S., Carninci P., Carninci P., Prange C.,
 RA Raha S.S., Louuellano N.A., Peters G.J., Abramson R.D., Mullahay S.J.,
 RA Bosak S.A., McWain P.J., McKernan K.J., Malek J.A., Gunnaraine P.H.,
 RA Richards S., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettlemen M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Rodriguez C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Mullahay S.J.,
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaraine P.H.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnurch A., Schein J.E.,
 RA Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RT and mouse cDNA sequences.",
 RT
 DR EMBL; BC054022; AAH54022.1; -.
 DR EMBL; BC054022; AAH54022.1; -.

DR InterPro; IPR008625; GAGE.
 DR Pfam; PF05831; GAGE; 1.
 SQ SEQUENCE 111 AA; 12090 MW; C0692E3DP2C905F8 CRC64;
 Best Local Similarity 31.1%; Score 169.5; DB 2; Length 111;
 Matches 45; Conservative 10; Mismatches 44; Indels 7; Gaps 3;
 Qy 4 RVSRSRGRGQBARPVAVFVARGE---SQEQQEPPTDNDQIEP-GQ-SERGTPIEE 56
 Db 6 RARSQSSERGNDQBSQPVGSVIVQEPTEKRGKEEPPTDNGQIAPSGEINQAVPAFQG 65
 Qy 57 RKVEGDCQEMDLEKTRSRSGDSDVKEKTPPNPKHAKTKEAGDGQP 102
 Db 66 PDMEAFQBLALKIEDPGGDPREGIMPTFDLTKVLEAGDAQP 111
 RESULT 4
 GGD5_HUMAN
 ID GGD5_HUMAN STANDARD; PRT; 108 AA.
 AC OBWWML;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 G antigen family D 5 protein (XAGE-5 protein).
 GN Name=GAGE5; Synonyms=XAGE5;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9605;
 RN [1] N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20031429; PubMed=11992404; DOI=10.1002/ijc.10371;
 RA Zendman A.J.W., Van Kraats A.A., Weidle U.H., Ruiter D.J.,
 RA Van Muilen G.N.P.,
 RT "The XAGE family of cancer/testis-associated genes: alignment and
 expression profile in normal tissues, melanoma lesions and Ewing's
 sarcoma.,"
 Int. J. Cancer 99:361-369(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heihe F.,
 RA Stapleton M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Datchenko D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Gabej J., Helton E., Kerttman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnecher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.,"
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC - SIMILARITY: Belongs to the GAGE family.
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DR EMBL; AJ318894; CAC83015.1; -.
 DR EMBL; BC069129; AAH69129.1; -.
 DR Genew; HGNC:3390; GAGE5.
 DR InterPro; IPR008625; GAGE.
 DR Pfam; PF05831; GAGE; 1.
 KW Multigene family Y.
 SQ SEQUENCE 108 AA; 12077 MW; E3CD91E5C9241628 CRC64;
 Best Local Similarity 30.2%; Score 163.5; DB 1; Length 108;
 Matches 35; Conservative 10; Mismatches 29; Indels 3; Gaps 1;
 Qy 29 EGQQEPPTDNDQIEPQORE--GTPPIERKVEGCGOEMDLEKTRSRSGDSDVKEKT 85
 Db 30 EFQQEPPTESQDHTPQKREDDQGAARIQVNLEADLQLBLSQSQTGECGDSPDVQCKI 89
 Qy 86 PPNPKHAKTKEAGDGQP 102
 Db 90 LPKSEQPKMPEGGEGKP 106

RESULT 5
 GGD4_HUMAN
 ID GGD4_HUMAN STANDARD; PRT; 111 AA.
 AC Q8WTP9; Q8WWS9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 G antigen family D 4 protein (Placenta-specific gene 6 protein) (XAGE-
 3 protein) (pp9012).
 GN Name=GAGE6; Synonyms=PLAC6, XAGE3;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9605;
 RN [1] N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22021429; PubMed=11992404; DOI=10.1002/ijc.10371;
 RA Zendman A.J.W., Van Kraats A.A., Weidle U.H., Ruiter D.J.,
 RA Van Muilen G.N.P.,
 RT "The XAGE family of cancer/testis-associated genes: alignment and
 expression profile in normal tissues, melanoma lesions and Ewing's
 sarcoma.,"
 Int. J. Cancer 99:361-369(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX Zhou X.M., Zhang P.P., Jiang H.Q., Huang Y., Qin W.X., Zhao X.T.,
 RA Wan D.F., Gu J.R.,
 RT "Novel human cDNA clones with function of inhibiting cancer cell
 growth.,"
 RT Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RT TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heihe F.,
 RA Datchenko D., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerttman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 RA Schnecher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human

RA Zendman A.J.W., Van Kraats A.A., Weidle U.H., Ruitter D.J.,
 RA Van Mulen G.N.P.;
 RT "The GAGE family of cancer/testis-associated genes: alignment and
 RT expression profile in normal tissues, melanoma lesions and Ewing's
 RT sarcoma;"
 Int. J. Cancer 99:361-369 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Murzny D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madden A., Rodriguez S., Sanchez A.,
 Whiting M., Madden A., Rodriguez S., Sanchez A.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
 Schnarch A., Schein J.E., Jones J.S.M., Marr M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences;"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Unknown.

CC -1- SIMILARITY: Belongs to the GAGE family.

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CC

DR EMBL: AJ318991; CAC88125.1; JOINED.

DR EMBL: AJ318992; CAC88125.1; JOINED.

CC EMBL: BC009322; AAH09322.1; -.

DR Genew; HGNC:4112; GAGED3.

MM: 300416; -.

DR InterPro:IPR008425; GAGE.

DR Pfam; PF05831; GAGE; 1.

KW Multigene family.

SQ SEQUENCE 111 AA; 12354 MW; 38C9332C5BA0E14 CRC64;

Query Match 24.3%; Score 131.5; DB 1; Length 111;
 Best Local Similarity 37.0%; Pred. No. 0.0021; Indels 40; Gaps 0;
 Matches Conservative 16; Mismatches 45; Indels 7; Gaps 3;

Oy 1 MSARVRS--RSRERGDPQEARPDYAFVAP--GSQOERPRPTDQDPIESPGQREB--GTPP 53
 Db 1 MSWRGRSRYPRPRRSLOPPELIGMLPTEPDKKEPKPSRNPTPDQKEDDQKAE 60

Oy 54 IEBRKVEGQOEMDLEKTRSERGDSYKEKUPPNPKAAKTKERAGDGQ 101
 Db 61 IQVpDLEADLQELCQTKTQGCGGGTVDKKGULPKAEEFKMPBAGECK 108

RESULT 8

O6NT33 PRELIMINARY; PRM; 117 AA.

ID Q6NT33; AC 06NT33; DT 05-JUL-2004 (Tremble. 27, Created)
 DT 05-JUL-2004 (Tremble. 27, Last sequence update)
 DT 05-JUL-2004 (Tremble. 27, Last annotation update)

DE DE Backer O., Arden K.C., Borotti M., Vantomme V., De Smet C.,
 RA Czeckay S., Viars C.S., De Paele E., Brasseur F., Chomez P.,
 RA Van den Eynde B., Boon T., van der Bruggen P.,
 RT "Characterization of the GAGE genes that are expressed in various
 RT human cancers and in normal testis.";

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=PCR rescued clones;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Murzny D.M., Sodegren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madden A., Rodriguez S., Sanchez A.,
 Whiting M., Madden A., Young A.C., Slezchko Y., Boutiffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
 Jones S.J., Marr M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences;"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RL [2]

RN RP SEQUENCE FROM N.A.

RC TISSUE=PCR rescued clones;

RA Strausberg R., Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

DR EMBL: BC069470; AAH69470.1; -.

DR InterPro: IPR00625; GAGE.

DR Pfam: PF05831; GAGE; 1.

SQ SEQUENCE 117 AA; 12885 MW; 3658D71B24DDC7AD CRC64;

Query Match 24.2%; Score 131; DB 2; Length 117;
 Best Local Similarity 40.5%; Pred. No. 0.0024; Indels 32; Gaps 1;
 Matches Conservative 7; Mismatches 38; Indels 2; Gaps 1;

Oy 25 VARGESDQEERPTDNDQDIEPGO--ERIGTPPERKTYEGDCOMDLKTRSRGDSDVK 82
 Db 36 VEPATPBPGEPATQDOPAAMAOBEGEDBGASAGQGPKEADSOBQHPTGTGCEDGPDGQ 95

Oy 83 EKPPNPNGHAKKEAGGQ 101
 Db 96 EMDPPNNPEEVKTPPEEGBQ 114

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9923383; PubMed=10397259;

RA De Backer O., Arden K.C., Borotti M., Vantomme V., De Smet C.,
 RA Czeckay S., Viars C.S., De Paele E., Brasseur F., Chomez P.,
 RA Van den Eynde B., Boon T., van der Bruggen P.,
 RT "Characterization of the GAGE genes that are expressed in various
 RT human cancers and in normal testis.";

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9923383; PubMed=10397259;

RA De Backer O., Arden K.C., Borotti M., Vantomme V., De Smet C.,
 RA Czeckay S., Viars C.S., De Paele E., Brasseur F., Chomez P.,
 RA Van den Eynde B., Boon T., van der Bruggen P.,
 RT "Characterization of the GAGE genes that are expressed in various
 RT human cancers and in normal testis.";

RN [1]

GN Name=GAGE4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;

RL. Cancer Res. 59:3157-3165 (1999).
 RN [2] SEQUENCE FROM N.A.
 RP TISSUE-Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hogenboom R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Steapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Utdin T.B., Toshimura K., Carninci P., Prange C.,
 RA Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibb R.A.,
 RA Fahney J., Heitman B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J.J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
 RA Scherich A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- TISSUE SPECIFICITY: Not expressed in normal tissues, except in
 CC testis, but expressed by a large proportion of tumors of various
 CC histological origins.
 CC -1- SIMILARITY: Belongs to the GAGE family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial/
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U19145; AAA82747.1; -.
 DR Genew; HGNC:4101; GAGE4.
 DR MMDB; 604245; -.
 DR InterPro; IPR008625; GAGE.
 DR PRam; PR0531; GAGE; 1.
 DR KW Multigene family; GAGE; 1.
 SQ SEQUENCE 117 AA; 12956 MW; 365BD71B2F9DC7AD CRC64;
 SQ
 Query Match 22.7%; Score 123; DB 1; Length 117;
 Best Local Similarity 39.2%; Pred. No. 0.01; Indels 2; Gaps 1;
 Matches 31; Conservative 7; Mismatches 39; Indels 2; Gaps 1;
 Qy 25 VAPGESQEEPTDNDIEPQQ-EERGTPIIERRKVEGQCOMDELEKTRSERGSDVK 82
 Db 36 VTPATPREGEGPATORDPAAQAGEDEGEDAGSAGQPKREADSOEQHQPOTGCCEDGPQQ 95
 Qy 83 EKKPPNKHAKTKREAGQ 101
 Db 96 ENDPPNPEEVKTPPEEGKQ 114
 RESULT 11
 GAGE5_HUMAN
 ID GAGE5_HUMAN STANDARD; FRT; 117 AA.
 AC 013069;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE GAGE-5 protein (G antigen 5).
 GN Name=GAGE5;
 OS Homo sapiens (Human).
 OC Bacteriota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9605;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=95378788; PubMed=7544395;
 RA van den Eynde B., Peeters O., de Backer O., Gaugler B., Lucas S.,
 RA Boon T.;
 RT A new family of genes coding for an antigen recognized by autologous
 RT cytolytic T lymphocytes on a human melanoma.;"
 RL J. Exp. Med. 182:689-698 (1995).
 RN [2] SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

OM protein - protein search, using BW model
Run on: August 24, 2005, 18:24:55 , Search time 71 Seconds
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Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

6: genebeGP2003ab; *
 7: genebeGP2003bs; *
 8: genebeGP2004bs; *

 KW PAGE-4; MAGE; GAGE; reproduction; testis; prostate; fallopian tube;
 KW uterus; placenta; cancer; major histocompatibility complex; MHC; CRL;
 KW cytotoxic T lymphocyte; immune response; antibody; drug delivery;
 KW immun conjugate.

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GenCore version 5.1.6

CC -4 or PAGE-4 peptide fragments can also be used in these compositions.
 CC Antibodies against PAGE-4 and its peptide fragments can be used in
 CC detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell
 CC samples or body tissues. The presence of PAGE-4 in tissues which are not
 CC related to reproduction can be indicative of the spread of cancerous
 CC reproductive tissue. PAGE-4 can also be used to raise antibodies which
 CC are then used as the targeting group of immunoconjugates comprising
 CC delivery systems
 XX Sequence 102 AA;

Query Match 100.0%; Score 541; DB 3; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSARVRSSRGRGDQAPDVAFVARGESQEEPPTDNQIEPGOBREGTPPIERKVE 60
 ID 1 MSARVRSSRGRGDQAPDVAFVARGESQEEPPTDNQIEPGOBREGTPPIERKVE 60
 AAY52998 standard; protein; 102 AA.

Db 61 GDCQEMDLEKTRSERGDSDVKEKTPPNPKHAKTEAGDQP 102

RESULT 2
 AAY52998
 ID AAY52998; XX
 AC AAY52998; XX
 DT 29-FEB-2000 (first entry)
 XX DE Human secreted protein clone bn365_53 protein sequence SEQ ID NO:2.
 KW Human; secreted protein; differentiation; immune stimulating; cytokine; cell proliferation;
 KW differentiation; immune stimulating; vaccine; suppression; haemopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokine; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour inhibition; gene therapy.
 KW tumour inhibition; gene therapy.
 OS Homo sapiens,
 XX PN W0957132-A1,
 XX PD 11-NOV-1999.
 XX PR 07 MAY 1998; 98US-0084564P. ←
 PR 02 JUN-1998; 98US-0087645P.
 PR 22-JUL-1998; 98US-0093712P.
 PR 31-JUL-1998; 98US-0094935P.
 PR 10-AUG-1998; 98US-009580P.
 PR 11-AUG-1998; 98US-009608P.
 PR 06-MAY-1999; 99US-00306111.

XX (GEMY) GENETICS INST INC.
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Bowman MR;
 PI DiBlasio-Smith E, Widom A;
 DR WPI, 2000-052937/04.
 DR N-PSDB; AA23316.

XX New polynucleotides encoding secreted human proteins, derived from adult
 PT placenta, adult retina, fetal brain, fetal.
 XX Claim 9; Page 360-361; 492pp; English.

CC The present invention describes new human secreted proteins which were

CC isolated from adult placenta, adult retina, foetal kidney, adult blood, adult brain, adult thyroid, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haemopoiesis regulating activity, tissue growth activity, actinin/inhibin activity, chemotactic/chamokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. AA23316 represent human secreted proteins, given in the present invention
 XX Sequence 102 AA;

Query Match 100.0%; Score 541; DB 3; Length 102; ✓
 Best Local Similarity 100.0%; Pred. No. 1.7e-49;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSARVRSSRGRGDQAPDVAFVARGESQEEPPTDNQIEPGOBREGTPPIERKVE 60
 ID 1 MSARVRSSRGRGDQAPDVAFVARGESQEEPPTDNQIEPGOBREGTPPIERKVE 60
 Db 61 GDCQEMDLEKTRSERGDSDVKEKTPPNPKHAKTEAGDQP 102

RESULT 3
 AAE14575
 ID AAE14575 standard; protein; 102 AA.
 AC AAE14575;
 DT 21-MAY-2002 (first entry)
 XX DE Human differentially expressed BPH protein JT463726.
 XX KW JT463726; prostate; benign prostatic hyperplasia; BPH; human; GAGE-like;
 XX PAGE-like.
 OS Homo sapiens.
 XX PN WO200210318-A2.
 XX PD 07-FEB-2002.
 XX PR 31-JUL-2001; 2001WO-US0233861.
 XX PR 31-JUL-2000; 2000US-0222039P.
 XX PPA (GENE-) GENE LOGIC INC.
 XX Munger WE, Kulkarni P, Getzenberg RH;
 XX DR WPI; 2002-206184/26.
 XX N-PSDB; AA24228.
 XX Claim 17; Page 48; 48pp; English.

PT Methods for diagnosing prostatic diseases in a patient, e.g. benign prostatic hyperplasia, or screening compounds for treating these diseases, comprises assaying for the expression of JT463725 protein or nucleic acid in a sample.

PS The invention relates to a method of diagnosing prostatic disease in a patient, which comprises assaying for the expression of JT463725 protein or nucleic acid in a sample. The differential expression of the protein or nucleic acid compared to normal prostate tissue is an indication of

CC prostatic disease. The method is useful for diagnosing prostatic
 CC diseases, particularly benign prostatic hyperplasia (BPH). The method is
 CC also useful for screening agents useful in treating BPH, isolating
 CC binding partners that bind to the proteins and for screening novel
 CC therapeutics that regulate prostate function. The genes and proteins are
 CC useful as diagnostic agents or markers for detecting BPH or the
 CC progression of BPH in a subject. They can also serve as a target for
 CC agents that modulate gene expression or activity. The present sequence is
 CC human JY46326 shows homology to GAGE/PAGE-like protein
 CC JY46326 shows homology to GAGE/PAGE-like protein
 XX SQ Sequence 102 AA;

Query Match 100.0%; Score 541; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Db 1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Db 61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

RESULT 4
 ADB75362
 ID ADB75362 standard; protein; 102 AA.
 XX AC ADB75362;
 XX DT 04-DEC-2003 (first entry)
 XX DE Prostate cancer marker protein.
 XX KW Prostate; cancer; cytostatic; gene therapy; marker.
 OS Homo sapiens.
 PN WO2003009814-A2.
 XX PD 06-FEB-2003.
 XX PR 25-JUL-2002; 2002WO-US023913.
 XX PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.
 XX PA (MILL-) MILLENIUM PHARM INC.
 PI Schlegel R, Monahan JE, Bredge WO, Gannavarapu M, Gorbatcheva B;
 PI Hoerath S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
 XX DR WPI; 2003-248033/24.

XX PT New nucleic acid molecule, useful for diagnosing or treating prostate
 CC cancer.
 CC Disclosure: SEQ ID NO 186; 99pp; English.
 XX
 CC The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.

CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75361 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

SQ Sequence 102 AA;

Query Match 100.0%; Score 541; DB 7; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Db 1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Db 61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

RESULT 5
 ADL90086
 ID ADL90096 standard; protein; 102 AA.
 XX AC ADL90096;
 XX DT 17-JUN-2004 (first entry)
 XX DE Human prostate associated gene protein 4.
 XX KW Immune response; immunoglobulin; Ig; human;
 XX DE prostate associated gene protein 4.
 OS Homo sapiens.
 PN WO2004027049-A2.
 XX PD 01-APR-2004.
 PR 18-SEP-2003; 2003WO-US030188.
 PR 20-SEP-2002; 2002US-0412219P.
 PR 14-MAR-2003; 2003WO-US007995.
 XX PA (ASTR-) ASTRAL INC.
 PI Bot A, Wang L, Smith D, Phillips B;
 XX DR WPI; 2004-295415/27.
 XX PT Generating an immune response comprises administering an immunoglobulin having
 CC desired T cell responses. Comprises administering an immunoglobulin having
 CC one peptide epitope of the antigen attached to the immunoglobulin.
 CC Disclosure; Fig 1L; 154pp; English.
 XX
 CC The present invention relates to a method for generating an immune
 CC response to an antigen in a patient. The method comprises administering
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at
 CC least one peptide epitope of the antigen attached to the Ig or its
 CC portion and administering the immunoglobulin or its portion in
 CC conjunction with a RNA segment. The present sequence is an antigen
 CC sequence, used to illustrate the invention.
 XX SQ Sequence 102 AA;

Query Match 100.0%; Score 541; DB 8; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.7e-49; Mismatches 0; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Db 1 MSARVRSRGRGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Db 61 GDQEMPLEKTRSERGDSVKEKTPNPKHAKTEAGDQGP 102

Qy

RESULT 6

ID ADC42685
ID ADC42685 standard; protein; 99 AA.
XX
AC ADC42685;
XX DT 26-FEB-2004 (first entry)
XX DE Human PAGE-2 protein #4.
XX KW Human; NOVX; GAGE-like protein; interferon; GCR; mast cell protease; hepatocyte nuclear factor; cancer; immune disorder; hepatic disorder; trauma; HIV; Parkinson's disease; Alzheimer's disease.
XX OS Homo sapiens.
XX PN US2003-202971-A1.
XX PD 30-OCT-2003.
XX PF 06-MAY-2002; 2002US-00139854.
XX PR 15-FEB-2000; 2000US-0182723P.
PR 15-FEB-2000; 2000US-0182724P.
PR 15-FEB-2000; 2000US-0182733P.
PR 22-FEB-2000; 2000US-0183866P.
PR 23-FEB-2000; 2000US-0184215P.
PR 23-FEB-2000; 2000US-0184482P.
PR 23-FEB-2000; 2000US-0184497P.
PR 24-FEB-2000; 2000US-0184744P.
PR 13-APR-2000; 2000US-0197083P.
PR 10-AUG-2000; 2000US-0224157P.
PR 18-SEP-2000; 2000US-0233405P.
PR 27-SEP-2000; 2000US-0233605P.
PR 02-JAN-2001; 2001US-0259414P.
PR 18-JAN-2001; 2001US-0262454P.
PR 14-FEB-2001; 2001US-00783429.
XX PA (MAJU/) MAJUMDER K.
XX PT Majumder K;
XX DR WPI; 2003-900615/82.

RESULT 7

ID ADJ55754
ID ADJ55754 standard; peptide; 99 AA.
XX AC ADJ55754;
XX DT 06-MAY-2004 (first entry)
XX Peptide homologous to a fragment of a human NOV3 protein SeqID 46.
XX KW human; NOVX; neurogenesis; cell differentiation; cell motility; cell proliferation; haematoPOEsis; angiogenesis; proliferative disorder; cancer; mastocytosis; immune disorder; hepatic disorder; cirrhosis; viral infection; AIDS; hepatitis; neuro-olfactory; trauma; surgery; neoplastic; adenocarcinoma; lymphoma; asthma; Crohn's disease; multiple sclerosis; Albright hereditary osteodysplrophy; cytostatic; immunosuppressive; hepatotropic; Virucide; anti-HIV; anti-inflammatory; vulnerable; antiasthmatic; neuroprotective.
XX OS Homo sapiens.
XX PN US2003199465-A1.
XX PD 23-OCT-2003.
XX PR 22-APR-2002; 2002US-00131409.
XX PR 15-FEB-2000; 2000US-0182723P.
PR 15-FEB-2000; 2000US-0182724P.
PR 15-FEB-2000; 2000US-0182733P.
PR 22-FEB-2000; 2000US-0183866P.
PR 23-FEB-2000; 2000US-0184215P.
PR 23-FEB-2000; 2000US-0184497P.
PR 24-FEB-2000; 2000US-0184744P.
PR 13-APR-2000; 2000US-0197083P.
PR 03-JUL-2000; 2000US-0215855P.
PR 10-AUG-2000; 2000US-0224157P.
PR 18-SEP-2000; 2000US-0233405P.
PR 27-SEP-2000; 2000US-0236060P.
PR 02-JAN-2001; 2001US-0259414P.
PR 18-JAN-2001; 2001US-0262454P.
PR 14-FEB-2001; 2001US-00783429.
PR 03-JUL-2001; 2001US-00898953.
XX PA (MALY/) MALYANKAR U M.
PA (TCHER/.) TCHERNEV V T.
PA (PADI/.) PADIGARU M.
PA (TAUP/) TRUPIER R J.

NOVX and for identifying a potential therapeutic agent for use in treatment of a pathology, where the pathology is related to aberrant expression or aberrant physiological interaction of NOVX. NOVX NA or the antibody is useful for treating or preventing a pathology associated with NOVX e.g. cancer, immune disorder, hepatic disorder, trauma, HIV, Parkinson's disease, and Alzheimer's disease. The present sequence represents a protein showing sequence similarity to a NOVX protein (or fragment).

Sequence 99 AA;

Query Match 97.6%; Score 528; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 4e-48; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 99; Conservative 0; DDBJ 60
QY 4 RVRSRGRGRGQBARPDWAVAPGESQBERPTNDQDIEPGQBERGTPPIERKVEGDC 63
Db 1 RVRSRGRGRGQBARPDWAVAPGESQBERPTNDQDIEPGQBERGTPPIERKVEGDC 60
QY 64 QBMDELKTRSERGDSDVKSKTPPNPKHAKTKEAGDQP 102
Db 61 QBMDELKTRSERGDSDVKSKTPPNPKHAKTKEAGDQP 99

PA (SPYTK/) SPYTEK K A.
 PA (GUOK/) GUO X.
 PA (SPAD/) SPADERNA S K.
 PA (BOLD/) BOLDOG F L.
 PA (GERL/) GERLACH V.
 PA (ELBR/) ELLERMAN K.
 PA (MACD/) MACDOUGALL J R.
 PA (SMIT/) SMITHSON G.
 XX
 PI Malvankar UM, Tchernev VT, Padigaru M, Taupier RJ, Spytek KA, Macdougall JR;
 PI Guo X, Spaderna SK, Boldog FL, Gerlach V, Ellerman K, Macdougall JR;
 PI Smithson G;
 XX
 DR WPI; 2003-900202/82.

PT New polypeptides useful for treating e.g. cancer and mastocytosis, immune disorders, hepatic disorders, viral infections, asthma.
 PT XX
 PS Disclosure; SEQ ID NO 46; 86pp; English.

CC This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.
 CC Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel CC human NOX protein, as well as methods to identify small molecules that can be used to modulate or inhibit various processes including CC neurogenesis, cell differentiation, cell motility, cell proliferation, haemopoiesis and angiogenesis. Furthermore, they can be used in the manufacture of medicaments to treat proliferative disorders (e.g. cancer and mastocytosis), immune disorders, hepatic disorders (e.g. cirrhosis), viral infections (e.g. AIDS and hepatitis), disorders of the neuro-olfactory system (e.g. trauma, surgery, and/or neoplastic disorders), adenocarcinoma, lymphoma, asthma, Crohn's disease, multiple sclerosis and also for treating Albright hereditary osteodystrophy. Accordingly, they exhibit cytostatic, immunosuppressive, virucide, anti-HIV, antiinflammatory, pulmonary, antiasthmatic and neuroprotective activities. This peptide is homologous to a fragment of a human NOX protein of the invention.

XX Sequence 99 AA;

Query Match 97.6%; Score 528; DB 7; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4e-48; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RVRSRSRGDGQEAEPDVVAFVARGESQQEERTPDNQIEPGRECIPPIERKAVADC 63
 Db 1 RVRSRSRGDGQEAEPDVVAFVARGESQQEERTPDNQIEPGRECIPPIERKAVADC 60

Qy 64 QEMDLKTRSERGDSVKEKTPPNPKHAKTKEAGDQP 102
 Db 61 QEMDLKTRSERGDSVKEKTPPNPKHAKTKEAGDQP 99

RESULT 8
 ADM76592 ID ADM76592 standard; protein: 99 AA.
 AC ADM76592;
 XX DT 03-JUN-2004 (first entry)
 XX DE Human Nov3 protein-related protein fragment SeqID46.
 XX KW NOX; Cytostatic; immunosuppressive; virucide; anti-HIV; hepatotrophic; antiinflammatory; neuroprotective; nortropic; antiparkinsonian; gene therapy; vaccine; NOX-associated disorder; cancer; immune disorder; viral infection; AIDS; hepatitis; neurological disorder; Alzheimer's disease; Parkinson's disease; olfactory disorder; chromosome mapping; tissue typing; NOV3; human.
 XX KW

OS Homo sapiens.
 XX WO2004009634-A2.
 XX PR 04-OCT-2000; 2000US-0237862P.
 XX PR 02-JAN-2001; 2001US-0259414P.
 XX PR 18-JAN-2001; 2001US-0262454P.
 XX PR 14-FEB-2001; 2001US-00783449.
 XX PR 03-JUL-2001; 2001US-0089853.
 XX PR 03-OCT-2001; 2001US-00970607.

XX PA (CURA-) CURAGEN CORP.
 PI Gerlach VL, Ellerman K, Macdougall JR, Smithson G, Shimkets RA;
 PI Rastelli L, Herrmann J;
 XX DR WPI; 2004-143267/14.

PT New NOX polypeptides and nucleic acid molecules useful for diagnosing, preventing or treating NOX-associated disorders (e.g. cancer, AIDS or Alzheimer's disease), and in chromosome mapping, tissue typing or pharmacogenomic.

PT XX Disclosure; SEQ ID NO 46; 173pp; English.

CC This invention relates to novel NOX polypeptides and the DNA sequences which encode them. The invention may be useful for the development of compounds with a cytostatic, immunosuppressive, virucide, anti-HIV, hepatotropic, antiinflammatory, neuroprotective, nortropic or anti-parkinsonian activity. In addition, the disclosed sequences may be useful for gene therapy or development of a vaccine. The NOX polypeptide, nucleic acid or antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. These are used in diagnosing, treating or preventing NOX-associated disorders such as cancer, immune disorders, viral infections (for example AIDS or hepatitis), neurological disorders (for example Alzheimer's disease or Parkinson's disease) or olfactory disorders. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is that of a human protein fragment which was used to demonstrate homology between the NOX proteins of the invention and other human proteins.

XX Sequence 99 AA;

Query Match 97.6%; Score 528; DB 8; Length 99;
 Best Local Similarity 100.0%; Pred. No. 4e-48; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RVRSRSRGDGQEAEPDVVAFVARGESQQEERTPDNQIEPGRECIPPIERKAVADC 63
 Db 1 RVRSRSRGDGQEAEPDVVAFVARGESQQEERTPDNQIEPGRECIPPIERKAVADC 60

Qy 64 QEMDLKTRSERGDSVKEKTPPNPKHAKTKEAGDQP 102
 Db 61 QEMDLKTRSERGDSVKEKTPPNPKHAKTKEAGDQP 99

RESULT 9
 ID AAY12447 standard; protein: 89 AA.
 AC AAY12447;
 XX DT 17-JUN-1999 (first entry)
 XX DE Human 5' EST secreted protein SEQ ID NO:478.
 XX KW Human; secreted protein; EST; expressed sequence tag; diagnosis;

KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haemopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX OS Homo sapiens.
XX PN WO9906548-A2.
XX PD 11-FEB-1999.
XX PF 31-JUL-1998; 99WO-IB001222.
XX PR 01-AUG-1997; 97US-00905135.
XX PA (GST) GENSET.
XX PI Dumas Milne Edwards J, Ducleart A, Lacroix B;
XX PT WPI; 1999-153778/13.
XX DR N-PSDB; AAX1280.
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.
PS Claim 27; Page 778; 824pp; English.
CC AAX41094 to AAX1347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY1261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokeratin activity, cell
CC proliferation/differentiation activity, haemopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX Sequence 89 AA;
SQ Query Match 77.4%; Score 419; DB 2; Length 89;
Best Local Similarity 98.8%; Pred. No. 1.3e-36; Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 VVAFVAPGESQQESEPTDNDQIDPGQEREGTPPIERKVEGQDCQENDLEKTRSERGDSD 80
Db 8 VVAFVAPGESQQESEPTDNDQIDPGQEREGTPPIERKVEGQDCQENDLEKTRSERGDSD 67
QY 81 VIEKTPRNPKHAKTKAEAGD 100
Db 68 VIEKTPRNPKHAKTKAEAGD 87
RESULT 10
AYB3167
ID AYB3167 standard; protein; 87 AA.
XX
AC AYB3167;
XX
DT 24-JUL-2000 (first entry)
DE PAGE1 polypeptide.
XX
KW PAGE-4; MAGB; GAGE; reproduction; testis; prostate; fallopian tube;

KW uterus; placenta; cancer; major histocompatibility complex; MHC; CTL;
KW cytotoxic T lymphocyte; immune response; antibody; drug delivery;
KW immunocconjugate.
XX OS Homo sapiens.
XX PN WO200012706-A1.
XX PD 09-MAR-2000.
XX PF 31-AUG-1999; 98US-0098993P.
XX PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Pastan I, Brinkmann U, Vasmatzis G, Lee B;
XX DR WPI; 2000-237869/20.
XX Isolated PAGE-4 protein and peptide used for inducing a cytotoxic T
PR lymphocyte response and for raising antibodies which can be used to
PT detect the presence of PAGE-4 in cell samples or body tissues.
XX Disclosure; Fig 1b; 63pp; English.
CC PAGE-4 is a gene preferentially expressed in normal male and female
CC reproductive tissues e.g. prostate, testis, fallopian tube, uterus and
CC placenta, as well as in prostate cancer, testicular cancer and uterine
CC cancer. This expression pattern makes it a target for diagnosis and for
CC vaccine based therapy of such neoplasms. An isolated PAGE-4 peptide which
CC induces a cytotoxic T lymphocyte response when bound to a major
CC histocompatibility complex (MHC) class I molecule or the isolated PAGE-4
CC protein can be used in immunogenic compositions to raise a cytotoxic T
CC lymphocyte response against cells expressing PAGE-4 including cancer
CC cells of the prostate, uterus and testis. The nucleic acids encoding PAGE
CC -4 or PAGE-4 peptide fragments can also be used in these compositions.
CC Antibodies against PAGE-4 and its peptide fragments can be used in
CC detecting the presence of PAGE-4 and PAGE-4 coding sequences in cell
CC samples or body tissues. The presence of PAGE-4 in tissues which are not
CC related to reproduction can be indicative of the spread of cancerous
CC reproductive tissue. PAGE-4 can be used to raise antibodies which
CC are then used as the targeting group of immunoconjugates comprising
CC toxins used in therapeutic applications. This has applications for drug
CC delivery systems. This sequence is of the PAGE1 polypeptide which shares
CC sequence similarity with PAGE-4
XX Sequence 87 AA;
SQ Query Match 72.4%; Score 391.5; DB 3; Length 87;
Best Local Similarity 76.9%; Pred. No. 1e-33; Matches 80; Conservative 3; Mismatches 2; Indels 19; Gaps 2;
Matches 80; Conservative 3; Mismatches 2; Indels 19; Gaps 2;
QY 1 MSARYRSRSRGDGQEAQDPAVWVAFVAPGESQQESEPTDNDQIDPGQEREGTPPIERK 58
Db 1 MSARYRSRSRGDGQEAQDPAVWVAFVAPGESQQESEPTDNDQIDPGQEREGTPPIERK 58
QY 59 VEGDCQENDLEKTRSERGQDSVKEKTPRNPKHAKTKAEAGDQP 102
Db 49 QEDDAKTRSERGQDSVKEKTPRNPKHAKTKAEAGDQP 87
RESULT 11
ADJ3678
ID ADJ3678 standard; protein; 118 AA.
XX
AC ADJ3678;
XX
DT 22-APR-2004 (first entry)
XX
DE Protein of the invention SEQ ID NO:655.
XX
KW cytostatic; immunomodulator; antimicrobial; anti-inflammatory; pulmonary;

KW neuroprotective; gene therapy; cancer; bacterial infection;
 KW fungal infection; autoimmune disorder; inflammation; Parkinson's disease;
 XX allergy; wound healing; human.
 OS Homo sapiens.

FH
 PT Location/Qualifiers
 PT Misc-difference 42 /note= "Encoded by stop codon"
 PT Misc-difference 103 /note= "Encoded by stop codon"
 PT
 XX
 PN XX
 XX
 XX
 XX
 XX
 PR 18-MAY-2000; 2000US-00577408.
 PR 22-SEP-2000; 2000US-0067298.
 PR 24-OCT-2000; 2000US-00695781.
 PR 17-NOV-2000; 2000US-00715863.
 PR 01-FEB-2001; 2001US-00775330.
 PA
 XX
 XX
 PR (HYSE-) NYSEQ INC.
 XX
 PT Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Yang Y, Zhao QA, Goodrich RW, Liu C, Drmanac RT, Wehrman T, Chen R;
 DR WPI; 2002-062370/08.
 XX
 PT New polynucleotides for treating cancers, infection, autoimmune
 PT disorders, inflammations, Parkinson's disease, allergies or wounds, and
 PT for diagnostic or research methods.
 XX
 PS Disclosure; SEQ ID NO 655; 310pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide, which has a
 CC nucleotide sequence comprising one of 432 sequences described in
 CC specification (but not fully defined), or their mature protein coding
 CC portion, active domain coding portion or complementary sequences. A
 CC protein of the invention has cytostatic, immunomodulatory, antimicrobial,
 CC anti-inflammatory, vulnerary, and neuroprotective activity. A
 CC polynucleotide of the invention may have a use in gene therapy. The
 CC therapeutic (e.g. for treating cancers, bacterial or fungal infection,
 CC autoimmune disorders, inflammations, Parkinson's disease, allergies or
 CC wound), diagnostic and research methods. In particular, they are useful
 CC in antisense therapy, gene therapy, forensics, gene mapping,
 CC identification of mutations responsible for genetic disorders or other
 CC traits, to assess biodiversity, or to produce many types of data and
 CC products dependent on DNA and amino acid sequences. The polypeptides may
 CC be used to generate an antibody that specifically binds the polypeptide.
 CC These antibodies are useful for detecting or quantifying the polypeptide
 CC in the tissue. The polypeptides are also useful as molecular weight
 CC markers or as food supplements. The sequences shown in ADJ33672-ADJ33887
 CC represent proteins of the invention.
 XX
 Sequence 118 AA;

SQ Query Match 69.8%; Score 377.5; DB 5; Length 118;
 Best Local Similarity 80.6%; Pred. No. 4.5e-32; Matches 79; Conservative 1; Mismatches 13; Indels 5; Caps 3;

Qy 10 RGRGDQEA-PDVAFAVAPGE--SQQRSPPTQNDIPEGQERGTPPIERKVEGICQE 65
 Db 21 RGRGDGGGLPDVVAIPWPRPXLISQEEHHPINQDIEPGQERGTPPIERKVEGICQE 80

Qy 66 MDLEKTRSERGDSVSKETPPN-PKHAKTKEAGDQP 102
 Db 81 MDELKTRSERGDSVSKETPPNPKHAKTKEAGDQP 118

SQ Query Match 54.6%; Score 295.5; DB 3; Length 109;
 Best Local Similarity 61.5%; Pred. No. 2e-23; Matches 64; Conservative 4; Mismatches 31; Indels 5; Caps 1;

Qy 4 RVRSRGRGGQEAQDVAFVAPGE----SQQRSPPTQNDIPEGQERGTPPIERK 58
 Db 6 RARSOSSERGNDOQESQSPVGSVIVQEPTEERKQSEBPPTQNDISPGQERGTPPIERK 65

Qy 59 VEGDCQEMDLKTRSERGDSVSKETPPNPKHAKTKEAGDQP 102
 Db 66 VEGDCQEMALLKIEDFGDPDVREGIMPTFDLTKYVLEADAQP 109

presence or amount of NOVX NA in a sample, a pharmaceutical composition (comprising NOVX, NOVX NA or the antibody) and a kit comprising in one or more containers, NOVB and NOV10 are 2 of 13 disclosed NOVX proteins showing homology to GAGE (G-antigen) proteins (NOV1-4), interferons (NOVS and 6), G protein-coupled receptors (NOVR), mast cell proteases (NOVB and NOV10-12) and hepatocyte nuclear factors (NOV9). The antibody is useful for determining the presence or amount of NOVX in a sample. NOVX is useful for identifying an agent that binds to NOVX and for identifying a potential therapeutic agent for use in treatment of a pathology, where the pathology is related to aberrant expression or aberrant physiological interaction of NOVX. NOVX, NOVX NA or the antibody is useful for treating or preventing a pathology associated with NOVX e.g. cancer, immune disorder, hepatic disorder, trauma, HIV, Parkinson's disease, and Alzheimer's disease. The present sequence represents a protein showing sequence similarity to a NOVX protein (or fragment).

SQ Sequence 109 AA;

Query Match 54.6%; Score 295.5; DB 7; Length 109;

Best Local Similarity 61.5%; Pred No 2e-23; Mismatches 31; Indels 5; Gaps 1; Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;

Qy 4 RVRSRSGRGDGQAPDVAFVAPGE---SQEERPTNDQIEPQEREGTPPIERK 59
6 RARSOSBERGNDOBSSQPVGSVIVQEPTTEKROQEEPTNDQIEPQEREGTPPIERK 65
Qy 59 VEGDCQMDLEKTRSERGGDSVKEKTPPNPKHAKKEAGDQP 102
Db 66 VEGDCQMDLEKTRSERGGDSVKEKTPPNPKHAKKEAGDQP 109

RESULT 15

ADJ55845 standard; peptide; 109 AA.

ID ADJ55845; AC AC;
XX DT 06-MAY-2004 (first entry)

Peptide homologous to a fragment of a human NOV1 protein SeqID 28.
XX
XX
XX
DE human; NOVX; neurogenesis; cell differentiation; cell motility; cell proliferation; haemopoiesis; angiogenesis; proliferative disorder; cancer; mastocytosis; immune disorder; hepatic disorder; cirrhosis; viral infection; AIDS; hepatitis; neuro-olfactory; trauma; surgery; neoplastic; adenocarcinoma; lymphoma; asthma; Crohn's disease; multiple sclerosis; Abright hereditary osteodystrophy; cytotoxic; immunosuppressive; hepatotropic; viricide; anti-HIV; antiinflammatory; vulnerability; antiasthmatic; neuroprotective.
XX
OS Homo sapiens.
XX
PN US2001199465-A1.
XX
PD 23-OCT-2003.
XX
PP 22-APR-2002; 2002US-00131409.
XX
PR 15-FEB-2000; 2000US-0182723P.
PR 15-FEB-2000; 2000US-0182724P.
PR 15-FEB-2000; 2000US-0182733P.
PR 22-FEB-2000; 2000US-0183895P.
PR 23-FEB-2000; 2000US-0184275P.
PR 23-FEB-2000; 2000US-0184482P.
PR 24-FEB-2000; 2000US-0184497P.
PR 13-APR-2000; 2000US-0197083P.
PR 03-JUL-2000; 2000US-0215855P.
PR 10-AUG-2000; 2000US-0224157P.
PR 18-SEP-2000; 2000US-0233405P.
PR 27-SEP-2000; 2000US-0236060P.
PR 02-JAN-2001; 2001US-0259414P.

PR 18-JAN-2001; 2001US-0262454P.
PR 14-FEB-2001; 2001US-00783429.
PR 03-JUL-2001; 2001US-00898953.
XX
PA (NALY/) MALYANKAR U M.
PA (TCHE/) TCHERNEV V T.
PA (PAUL/) PAULIGARU M.
PA (TRUP/) TAUPIER R J.
PA (SPY/) SPYTEK K A.
PA (GUOK/) GUO X.
PA (SPAD/) SPADERNA S K.
PA (BOLD/) BOLDG F L.
(GERL/) GERLACH V.
(ELLE/) ELLERMAN K.
(MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
XX
PI Malayankar UM, Tchernev VT, Pedigaru M, Taupier RJ, Spytek KA,
Guo X, Spaderna SK, Boldog FL, Gerlach V, Ellerman K, Macdougall JR,
Smithson G;
XX
DR WPI; 2003-900202/82.
XX
PT New polypeptides useful for treating e.g. cancer and mastocytosis, immune disorders, hepatic disorders, viral infections, asthma.
XX
PS Disclosure; SEQ ID NO 28; 86pp; English.
CC This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.
CC Specifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays. The present invention describes novel CC diagnostic and prognostic assays. The present invention describes novel CC human NOVX proteins, as well as methods to identify small molecules that CC can be used to modulate or inhibit various processes including CC neurogenesis, cell differentiation, cell motility, cell proliferation, CC manufacture of medicaments to treat proliferative disorder (e.g. cancer CC and mastocytosis), immune disorders, hepatic disorders (e.g. cirrhosis), CC viral infections (e.g. AIDS and hepatitis), disorders of the neuro- CC olfactory system (e.g. trauma, surgery) and/or neoplastic disorders), CC adenocarcinoma, lymphoma, asthma, Crohn's disease, multiple sclerosis, and CC also for treating Abright hereditary osteodystrophy. Accordingly, they CC exhibit cytotoxic, immunosuppressive, hepatotropic, viricide, anti-HIV, CC antiinflammatory, vulnerary, antiasmotic and neuroprotective CC activities. This peptide is homologous to a fragment of a human NOVX CC protein of the invention.
XX
SQ Sequence 109 AA;

Query Match 54.6%; Score 295.5; DB 7; Length 109;

Best Local Similarity 61.5%; Pred No. 2e-23; Mismatches 31; Indels 5; Gaps 1; Matches 64; Conservative 4; Mismatches 31; Indels 5; Gaps 1;

Qy 4 RVRSRSGRGDGQAPDVAFVAPGE---SQEERPTNDQIEPQEREGTPPIERK 59
6 RARSOSBERGNDOBSSQPVGSVIVQEPTTEKROQEEPTNDQIEPQEREGTPPIERK 65
Qy 59 VEGDCQMDLEKTRSERGGDSVKEKTPPNPKHAKKEAGDQP 102
Db 66 VEGDCQMDLEKTRSERGGDSVKEKTPPNPKHAKKEAGDQP 109

Search completed: August 24, 2005, 18:42:12
Job time : 74 secs

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Q	67	DIEKTRSERGDCQMDLEKTRSERGDSVKEKTPNPKHAKTKEAGDGP	102
Db	542	--KGEPPEKGKGSVKEEGGPBKGKDGKVKEKG-GPP	574
RESULT 9	T52485	neurofilament protein NF-M(2'), middle molecular weight [imported] - African clawed frog	
C;Species:	Xenopus laevis (African clawed frog)		
C;Date:	24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004		
C;Accession:	T52485		
A;Title:	Toxoplasma gondii rhotrypt protein associated with host cell penetration has u		
A;Reference number:	A45644; MUID:92178277; PMID:1542304		
A;Accession:	A45644		
A;Molecule type:	mRNA		
A;Residues:	MACRQLCLSVQNLLPFLRADYCTDFR'		
A;Cross-references:	EMBL:MT1274; NID:9897822		
A;Note:	Sequence extracted from NCBI backbone (NCBIN:85178, NCBIP:85179)		
C;Superfamily:	surface protein rhotrypt		
C;Keywords:	surface antigen		
F;1-21;Domain:	signal sequence #status predicted <SIG>		
F;22-396;Product:	surface protein rhotrypt #status predicted <MAT>		
Query Match	16.5%	Score 89; DB 1; Length 96;	
Best Local Similarity	30.2%	Pred. No. 2.2; Gaps 5;	
Matches	32;	Conservative 15; Mismatches 37; Indels 22;	
Oy	16	QEAPDVVAFVAGCESQ-----QEPEPTDNQDIEPGQEREGTPPIE--RKVEG---- 61	
Db	143	QELPDGSLVERPENAPQELRPPPNVQELPPTEBLPLPSTEQELAPPVQEGQLQVPHGP 202	
Oy	62	-----QEDMLEKTRSRGDSVKEKTPNPKHAKTKEAGDGP 102	
Db	203	QGPYPYDQDQQLLSPTR-EQQEGP- QELPLPPPPTGEQPEGQQP 245	
RESULT 8	832103	filenin - bovine	
N;Alternate names:	intermediate filament protein		
C;Species:	Bos primigenius taurinus (cattle)		
C;Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Sep-1997		
C;Accession:	S32103; A40690		
C;Gounari, F.; Merdes, A.; Quinlan, R.; Hebs, J.; Fitzgerald, P.G.; Ouzounis, C.: Georgia submitted to the EMBL Data Library, March 1993			
A;Description:	Bovine filenin possesses primary and secondary structure similarity to 1		
A;Reference number:	S32103		
A;Accession:	S32103		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-755 <GO>		
A;Cross-references:	EMBL:X72388; NID:9287751; PID:9287752		
A;Title:	Bovine filenin possesses primary and secondary structure similarity to interme		
A;Reference number:	A40690; MUID:93260017; PMID:8491777		
A;Accession:	A40690		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-622, 'RP', 625-755, <GO>		
A;Experimental source:	lens		
A;Note:	Sequence extracted from NCBI backbone (NCBIN:132495, NCBIP:132499)		
A;Note:	part of this sequence was confirmed by protein sequencing		
C;Keywords:	membrane-associated protein		
Query Match	16.3%	Score 88; DB 2; Length 755;	
Best Local Similarity	34.0%	Pred. No. 5; Mismatches 6; Gaps 6;	
Matches	33;	Conservative 6; Mismatches 34; Indels 24; Gaps 6;	
Oy	12	RGPQEQARDVVAFVAGCSESQQRSPPTDNQDIEPGQEREGTPPIE--RKVEG---- 53	
Db	496	KGDPSVPPDSGVBPSP--QOBPPPLERGQGPQKEKGDKLKEBGGPP-----EG---- 541	
RESULT 10	E89066	protein H05C09.1 [imported] - Caenorhabditis elegans	
C;Species:	Caenorhabditis elegans		
C;Date:	10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004		
C;Accession:	E89066		
R;Anonymous:	The C. elegans Sequencing Consortium.		
A;Title:	Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology		
A;Reference number:	A75000; MUID:9969613; PMID:9881916		
A;Note:	See websites genome.wustl.edu/gse/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/		
A;Note:	published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and		
A;Accession:	E89066		
A;Status:	preliminary		
A;Molecule type:	DNA		
A;Residues:	1-2109 <GO>		
A;Cross-references:	UNIPROT:Q81SF7; UNIPROT:Q81SF6; UNIPROT:Q81SF5; GB:chr_V; PIDN:AAC119		
C;Genetics:	H05C09.1		
A;Map position:	5		
Query Match	16.3%	Score 88; DB 2; Length 2109;	
Best Local Similarity	29.4%	Pred. No. 14; Mismatches 8; Gaps 47; Indels 22;	
Matches	32;	Conservative 8; Mismatches 47; Indels 22; Gaps 3;	
Oy	16	QEAPDVVAFVAGCSESQQRSPPTDNQDIEPGQEREGTPPIE--REGTP-----P 53	
Db	1712	QGPYVMAPLERIQTQEEVKPKEAMIPSEPTQBDPKGAAPLEPTQDVPKGAAPSGPTQBDV 1771	
Oy	54	IRERKVQEGDCQMDLEKTRSERGDSVKEKTPNPKHAKTKEAGDGP 102	
Db	1772	KRAPSPTQEDVPKKAAPSEPTQENVPKEAAPSEPTKDVPKEAAPSE 1820	

T33247 hypothetical protein H05009.1 - *Caenorhabditis elegans* (fragment)

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

R;Leonard, S.; Hinds, K.

R;Submitted to the EMBL Data Library, May 1998

A;Description: The sequence of *C. elegans* cosmid H05009.

A;Reference number: 221308

A;Accession: T33247

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2109 <LEO>

A;Cross-references: UNIPROT:Q81SF7; UNIPROT:Q81SF6; UNIPROT:Q81SF5; EMBL:AT067951; PIDN:

A;Experimental source: strain Bristol N2; clone H05009

C;Genetics:

A;Gene: CEGP:H05009.1

A;Map position: 5

A;Note: intron positions not resolved (incomplete sequence)

Query Match 16.3%; Score 88; DB 2; Length 2109;

Best Local Similarity 29.4%; Pred. No. 14; Mismatches 8; Indels 22; Gaps 3;

Matches 32; Conservative 8; Mismatches 47; Indels 22; Gaps 3;

OY 16 QEPADPVVA-----FVARGESQEEPPPTNDQDIEP3QK--REGT-----P 53

Db 1712 Q3VPVMVAPLEPIQEEVVKPEAARSEPTQEDVPKGAAPLEPTQEDVPKAAAPSGPTQEDV 1771

OY 54 I8ERKVVEGDCQEMDLEKTRSERGDGSVDKVKTPPNPKHAKTKRAGDQ 102

Db 1772 KEBAPSPQTQEDVPKAAAPSEPTQENVPKAAAPSEPTKDVPKAAAPSEP 1820

RESULT 12

S20248 transcription factor TFIIF large chain - human

N;Alternate names: ATP-dependent DNA helicase RAP30/74 chain RAP4; RNA polymerase II-as

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S20248; S25402; S2503

R;Abo, T.; Vabava, H.A.; Kawaguchi, T.; Germino, F.J.; Ganguly, S.; Kitajima, S.; Weis

A;Title: Characterization of cDNA for the large subunit of the transcription initiation

A;Reference number: S20248; MUID:92131135; PMID:1734283

A;Accession: S20248

A;Molecule type: mRNA

A;Residues: 1-517 <AS01>

A;Cross-references: UNIPROT:P35269; EMBL:X64037; NID:915868; PIDN:CAA45408.1; PID:93869

A;Accession: S25402

A;Molecule type: protein

A;Residues: 27-4091-97-445-460-505-517 <AS02>

A;Finkelstein, A.; Kostrib, C.F.; Li, J.; Chavez, D.P.; Wang, B.Q.; Fang, S.M.; Greenbla

Nature 335, 464-467, 1992

A;Title: A cDNA encoding RAP74, a general initiation factor for transcription by RNA pol

A;Reference number: S20589; MUID:92131136; PMID:1734284

A;Accession: S20589

A;Molecule type: mRNA

A;Residues: 1-230; 'I', 232-360; 'L', 362-517 <FIN1>

A;Cross-references: EMBL:X64002; NID:935870; PIDN:CAA45404.1; PID:935871

A;Accession: S25403

A;Molecule type: protein

A;Residues: 35-4550-68-90-100-154-163;383-394;426-434 <FIN2>

C;Keywords: DNA binding; transcription regulation

Query Match 16.2%; Score 87.5; DB 2; Length 517;

Best Local Similarity 29.9%; Pred. No. 3; 8; Mismatches 44; Indels 27; Gaps 6;

Matches 35; Conservative 11; Mismatches 44; Indels 27; Gaps 6;

OY 9 SRGRGDQBAPDVAVFAVPGESQEEERP--TDNQDIEPGQEREGTPPIEERVKVEG-----62

Db 275 SPSQSSQEEPEPKA-KAP--QOECPKGIVDEQSDBEEBEEKEPKPDEDEEEKKAP 330

OY 63 COEMDLEKTRSERGQDSD-----VKEKTPP--NPKHAKTKRAGDQ 102

Db 331 TPQEKKRKQSEESDSSESDIDSEASSAFFMAKKCTPPKRERKPSGSSRGNSRP 387

RESULT 13

I50479 neurofilament medium protein - goldfish

C;Species: Carassius auratus (goldfish)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: I50479

R;Glasgow, E.; Hall, C.M.; Schechter, N.

J;Neurochem. 63, 52-61, 1994

A;Title: Organization, sequence, and expression of a gene encoding goldfish neurofilamen

A;Reference number: I50479; MUID:94267484; PMID:8207446

A;Accession: I50479

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-798 <GLA>

A;Cross-references: UNIPROT:Q90307; GB:L09742; NID:9213019; PIDN:AAA72341.1; PID:9213020

A;Introns: 343/3; 385/2

C;Superfamily: cytoskeletal keratin

Query Match 16.1%; Score 87; DB 2; Length 798;

Best Local Similarity 26.2%; Pred. No. 6.5; Mismatches 35; Indels 22; Gaps 4;

Matches 27; Conservative 19; Mismatches 35; Indels 22; Gaps 4;

OY 13 GDQEARPD-----VAFVARGESQEEPPPTNDQDIEPG---QEREGTPPIERK 58

Db 484 GEGERGEGEREEREVWSSQAKVAGSAPEDEGEKEGEKEBEAGKGEDEREGEGEEBEEK 543

OY 59 VEGDCQEMDIEKTRSERGDGSVDKVKTPPNPKHAKTKRAGDQ 101

Db 544 QEDDAEE-EAEETKAP-----EAKASPETEKAQEKPQSGGE 578

RESULT 14

T13161

A-kinase anchor protein 95 - human

C;Species: Homo sapiens (man)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T13161; T08786

R;Lamerdin, J.B.; McCready, P.M.; Skowronski, E.; Viswanathan, V.; Burkhardt-Schultz, K.;

J.; Dangaran, L.; Erler, A.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix,

; Quan, G.; Kronmiller, B.; Arellano, A.; Saunders, C.; Ow, D.; Nolan, M.; Trong, S.

B;Submitted to the EMBL Data Library, October 1998

A;Authors: Kobayashi, A.; Olsen, A.S.; Carrano, A.V.

A;Description: Sequence analysis of a 1.5 Mb OLFR-rich region in 19p13.1.

A;Reference number: Z17617

A;Accession: T13161

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-692 <AM>

A;Cross-references: UNIPROT:O43823; EMBL:AC005795; NID:9302290; PID:93702291; PIDN:AAC6

A;Koehler, K.; Beyer, A.; Mewes, H.W.; Gabenhuber, J.; Wiemann, S.

A;Submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16468

A;Accession: T08786

A;Molecule type: mRNA

A;Residues: 335-692 <KOB>

A;Cross-references: EMBL:AL05160

A;Experimental source: adult uterus; clone DKFZp586B1222

C;Genetics:

A;Map position: 19

A;Introns: 7/1; 20/1; 31/1; 124/2; 287/3; 331/1; 346/3; 358/1; 387/2; 434/3; 466/1; 509/

A;Note: DKFZp586B1222.1

Query Match 15.9%; Score 86; DB 2; Length 692;

Best Local Similarity 27.8%; Pred. No. 6.8; Mismatches 42; Indels 10; Gaps 3;

Matches 27; Conservative 18; Mismatches 42; Indels 10; Gaps 3;

OY 1 MSARVRSSRGDQGAPDVAVFVGESQEEERPPTNDQDIEPGQEREGTPPIERVKVE

RESULT 15
 D85135 ::|::|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 hypothetical protein At4g12610 [imported] - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C.Accession: D85135
 R. anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
 A.Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A.Reference number: A85001; MUID:20083488; PMID:10617198
 A.Accession: D85135
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-649 <STO>
 A.Cross-references: UNIPROT:Q9SU25; GB:NC_001268; NID:97267963; PIDN:CAB78304.1; GSPPB:G
 C.Gene: At4g12610
 A.Map position: 4

Query Match 15.7%; Score 85; DB 2; Length 649;
 Best Local Similarity 28.6%; Pred. No. 7-8;
 Matches 26; Conservative 17; Mismatches 42; Indels 6; Gaps 3;
 C.Qry ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 C.Db DGOBAPDVVA--FVAPGGSQERPTDQDIEPGQEREGTPPIERKVEGDCQEMDEKT 71
 C.Qry 14 303 DPBEREDLIAKEPTEIAPPETIKQDEDDEENEEBEGGLSKSGK--ELKKUIGKANGLD-ESD 358
 C.Db 72 RSRBGDGSPVKEKPPRNPGAKAKEAGQQP 102
 C.Qry 359 EDDDDSDPDEEETNYGTWINSKOKEAKEEP 389

Search completed: August 24, 2005, 18:43:43
 Job time : 23 secs

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Run on:	August 24, 2005, 18:41:17 ;	Search time 42 Seconds	181.291 Million cell updates/sec
OM protein - protein search, using SW model			
Title:	US-09-763-393-1		
Perfect score:	541		
Sequence:	1 MSARVRSRSGRGDQEAPD..... EKTPPNPKHAKTKERAGDGQP 102		
Scoring table:	BLOSUM2		
gapop 10.0 , Gapext 0.5			
Searched:	513545 seqs, 74649064 residues		
Total number of hits satisfying chosen parameters:	513545		
Minimum DB seq length: 0			
Maximum DB seq length: 200000000			
Post-processing: Minimum Match 0%			
Listing first 45 summaries			
Database :			
Issued Patents AA:*			
1: /cgn2_6/ptodata/1/1aa/5A_COMBO.pep:*			
2: /cgn2_6/ptodata/1/1aa/5B_COMBO.pep:*			
3: /cgn2_6/ptodata/1/1aa/6A_COMBO.pep:*			
4: /cgn2_6/ptodata/1/1aa/6B_COMBO.pep:*			
5: /cgn2_6/ptodata/1/1aa/PC10S_COMBO.pep:*			
6: /cgn2_6/ptodata/1/1aa/backflesl.pep:*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
SUMMARIES			
Result No.	Score	Query Match Length	DB ID
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1	181.5	33.5	111 4 US-09-621-976-7591
2	181.5	33.5	111 4 US-09-621-976-7592
3	122	33.5	110 4 US-09-621-976-7592
4	107	19.8	116 4 US-09-163-748C-7
5	107	19.8	117 4 US-09-163-748C-7
6	106.5	19.7	1861 4 US-09-873-37A-6
7	93.5	17.3	1862 4 US-09-873-37A-4
8	93.5	17.3	392 3 US-08-301-162-2
9	93.5	17.3	392 3 US-09-461-240-2
10	93.5	17.3	428 3 US-08-301-162-18
11	93.5	17.3	428 3 US-09-461-240-18
12	93.5	17.3	428 4 US-09-968-27-18
13	93.5	17.3	667 3 US-09-303-064-55
14	93.5	17.3	667 3 US-09-303-064-55
15	87.5	16.2	517 4 US-09-949-016-6170
16	87.5	16.2	520 4 US-09-949-016-7728
17	85	15.7	5037 4 US-09-949-016-7728
18	84.5	15.6	2079 4 US-09-949-016-8301
19	83.8	15.5	437 4 US-09-253-911-28176
20	82.5	15.2	599 4 US-09-531-864
21	82.5	15.2	5032 4 US-09-538-092-979
22	82	15.2	701 4 US-09-252-911A-24048
23	81.5	15.1	565 4 US-09-252-911A-20122
24	81	15.0	263 4 US-09-902-50-11171
25	80.5	14.9	290 4 US-09-248-916A-14401
26	80.5	14.9	628 4 US-09-252-911A-24491
27	80	14.8	159 4 US-09-270-767-36313
ALIGNMENTS			
RESULT 1	US-09-621-976-7591		
;	Sequence 7591, Application US/09621976		
;	Patent No. 6639063		
;	GENERAL INFORMATION:		
;	APPLICANT: Dumas Milne Edwards, J.-B.		
;	APPLICANT: Giordano, J.Y.		
;	TITLE OF INVENTION: ESTs and Encoded Human Proteins.		
;	FILE REFERENCE: GENSET 054P12		
;	CURRENT APPLICATION NUMBER: US/09/621, 976		
;	CURRENT FILING DATE: 2000-07-21		
;	SEQUENCE ID NO: 7592		
;	SEQUENCE LENGTH: 111		
;	TYPE: PRT		
;	ORGANISM: Homo sapiens		
;	SOFTWARE: Patent.pm		
;	SEQ ID NO: 7591		
;	LENGTH: 111		
;	TYPE: PRT		
;	US-09-621-976-7591		
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;	Best Local Similarity 44.1%; Pred. No. 3e-12; Mismatches 42; Indels 9; Gaps 4;		
;	Matches 49; Conservative 11; Mismatches 42; Indels 9; Gaps 4;		
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;	Sequence 2, Appli		
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;	Sequence 7592, Application US/09621976		
;	Patent No. 6639063		
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;	Patent No. 6639063		
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;	Patent No. 6639063		
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;	Sequence 7591, Application US/09621976		
;	Patent No. 6639063		
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;	APPLICANT: Dumas Milne Edwards, J.-B.		
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;	TITLE OF INVENTION: ESTs and Encoded Human Proteins.		
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;	US-09-621-976-7591		
;	Sequence 7591, Application US/09621976		
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;	APPLICANT: Dumas Milne Edwards, J.-B.		
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;	TITLE OF INVENTION: ESTs and Encoded Human Proteins.		
;	FILE REFERENCE: GENSET 054P12		
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;	Patent No. 6639063		
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;	APPLICANT: Dumas Milne Edwards, J.-B.		
;	APPLICANT: Giordano, J.Y.		
;	TITLE OF INVENTION: ESTs and Encoded Human Proteins.		
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;	CURRENT FILING DATE: 2000-07-21		
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;	US-09-621-976-7591		
;	Sequence 7591, Application US/09621976		
;	Patent No. 6639063		
;	GENERAL INFORMATION:		
;	APPLICANT: Dumas Milne Edwards, J.-B.		
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;	TITLE OF INVENTION: ESTs and Encoded Human Proteins.		
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;	APPLICANT: Dumas Milne Edwards, J.-B.		
;	APPLICANT: Giordano, J.Y.		
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;	Patent No. 6639063		
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;	APPLICANT: Dumas Milne Edwards, J.-B.		
;	APPLICANT: Giordano, J.Y.		

Query Match 19.8%; Score 107; DB 4; Length 861;
 Best Local Similarity 28.3%; Pred. No. 0.0038; Indels 8; Gaps 3;
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Qy 53 PIBRKVECDQEMDLKTRSERGDGSVKEKTPPNPKHAKTEAG 98
 Db 61 KSOLOQISAGFOELSLAERGRRDFHDXGVNTRNLDHVKESKTG 106

RESULT 6 19.8%; Score 107; DB 4; Length 861;
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 ; Patent No. 6723534
 ; GENERAL INFORMATION:
 ; APPLICANT: Duke University
 ; INVENTOR: Lin, Haifan
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED piwi FAMILY GENES AND GENE
 ; TITLE OF INVENTION: PRODUCTS AND THERAPEUTIC AND SCREENING METHODS USING SAME
 ; FILE REFERENCE: Attorney Docket No. 6723534 180-104/2
 ; CURRENT APPLICATION NUMBER: US/09/873,737A
 ; CURRENT FILING DATE: 2001-06-04
 ; PCT/US99/28764
 ; PRIORITY NUMBER: 60/110,901
 ; PRIORITY FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4
 ; LENGTH: 862
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 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; NAME/KEY: mbc_feature
 ; LOCATION: (90)
 ; OTHER INFORMATION: Xaa-Leu or Ile
 ; NAME/KEY: mbc_feature
 ; LOCATION: (216)
 ; OTHER INFORMATION: Xaa-Leu or Ile
 ; NAME/KEY: mbc_feature
 ; LOCATION: (383)
 ; OTHER INFORMATION: Xaa-Leu or Ile
 ; NAME/KEY: mbc_feature
 ; LOCATION: (816)
 ; OTHER INFORMATION: Xaa-Leu or Ile
 ; US-09-873-737A-4

Query Match 19.7%; Score 106.5; DB 4; Length 862;
 Best Local Similarity 29.1%; Pred. No. 0.0043; Indels 15; Gaps 3;
 Matches 32; Conservative 15; Mismatches 48; ;

Qy 1 MSARVRSRGRGRGQEAAPDVVAFAVGEQQ-----ESPTNDIPEQER--- 48
 Db 1 MTGRARARAGRGRGQETQVLGVSTASQQGYIQPRPQSPTEGDVLGRGRGQMV 57

Qy 49 EGMPIPIERKVECDQEMDLKTRSERGDGSVKEKTPPNPKHAKTEAG 98
 Db 58 GATSKSOLQISAGFOELSLAERGRRDFHDXGVNTRNLDHVKESKTG 107

RESULT 7 19.8%; Score 107; DB 4; Length 861;
 US-08-301-162-2
 ; Sequence 2, Application US/08301162
 ; Patent No. 6025546
 ; GENERAL INFORMATION:
 ; APPLICANT: Knapp, Stefan
 ; APPLICANT: Ziegelemaier, Robert
 ; APPLICANT: Kupper, Hans
 ; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The Preparation Thereof and the Use Thereof
 ; TITLE OF INVENTION: Preparation Thereof and the Use Thereof

RESULT 8 17.3%; Score 93.5; DB 3; Length 392;
 US-09-461-240-2
 ; Sequence 2, Application US/09461240
 ; Patent No. 6726008
 ; GENERAL INFORMATION:
 ; APPLICANT: Knapp, Stefan
 ; APPLICANT: Ziegelemaier, Robert
 ; APPLICANT: Kupper, Hans
 ; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The Preparation Thereof and the Use Thereof
 ; TITLE OF INVENTION: Preparation Thereof and the Use Thereof

NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 COMPUTER READABLE FORM:
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 COMPUTER READABLE FORM:
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 COMPUTER READABLE FORM:

FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleschner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 02481.1.005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLogy: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-08-301-162-18
Query Match 17.3% Score 93.5; DB 3; Length 428;
Best Local Similarity 30.3%; Pred. No. 0 046; 3; Length 428;
Matches 30; Conservative 15; Mismatches 39; Indels 15; Gaps 4;
Qy 16 QEPADVAVFVGESQSERPPTNDQIPEPGCEREGTPIES--RKYEG-----DC 63
Db 182 QBLPPPTEQELPBPPTQBLPPPTEQELAPSTQEQLPPVGBCQRLOVPGEHGPQGPPYDD 241
Qy 64 QEMDLEKTRSERGDDGVKEKTPPNQGHAKTEAGIGQ 102
Db 242 QQLLLEPT-EQQEGL--QEPPLPPPPTRGEQPCQQP 277
RESULT 11
US-09-461-240-18
Sequence 18, Application US/09461240
; Patent No. 6326008
GENERAL INFORMATION:
APPLICANT: Knapp, Stefan
Ziegelmair, Robert
Kupper, Hans
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461-240
FILING DATE: 16-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/301,162
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/167,128
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleschner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 02481.1.005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TOPOLogy: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-461-240-18
Query Match 17.3% Score 93.5; DB 3; Length 428;
Best Local Similarity 30.3%; Pred. No. 0 046; 3; Length 428;
Matches 30; Conservative 15; Mismatches 39; Indels 15; Gaps 4;
Qy 16 QEPADVAVFVGESQSERPPTNDQIPEPGCEREGTPIES--RKYEG-----DC 63
Db 182 QBLPPPTEQELPBPPTQBLPPPTEQELAPSTQEQLPPVGBCQRLOVPGEHGPQGPPYDD 241
Qy 64 QEMDLEKTRSERGDDGVKEKTPPNQGHAKTEAGIGQ 102
Db 242 QQLLLEPT-EQQEGL--QEPPLPPPPTRGEQPCQQP 277
RESULT 12
US-09-968-927-18
Sequence 18, Application US/09968927
; Patent No. 6419925
GENERAL INFORMATION:
APPLICANT: Knapp, Stefan
Ziegelmair, Robert
Kupper, Hans
TITLE OF INVENTION: Toxoplasma Gondii Antigens, The Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,927
FILING DATE: 03-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/301,162
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/167,128
FILING DATE: <Unknown>
APPLICATION NUMBER: US/07/623,086
FILING DATE: 06-DEC-1990
APPLICATION NUMBER: DE P3940598.2
FILING DATE: 08-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleschner, Raz E.
REGISTRATION NUMBER: 34,331
REFERENCE/DOCKET NUMBER: 02481.1.005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400

US-09-968-927-18

Query Match 17.3%; Score 93.5; DB 4; Length 428;
 Best Local Similarity 30.3%; Pred. No. 0.046; Matches 30; Conservative 15; Mismatches 39; Indels 15; Gaps 4
 Qy 16 QEAPDVAVFVARGESQEEBPITDNDQDIEPGQERGTPPIEE--RKTEG-----DC 63

182 OELPPPTEOELPPPTEOELPPPTEOELAPSSITEOELPPVGEGORLOVPGEHEKPOGPPYDD 241 Db

QY	64 OEMDLEKTRSERGDSVKEPTPPNKHAKTKEAGCQP	1022
Db	242 QQLLERT-EBQEQP--QEPLUPPPPPPTRGQBPEGCQP	2777

; CURRENT APPLICATION NUMBER: US/09/086,503A
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 55 ; LENGTH: 667
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-086-503-55

APPLICANT: BROJANAC, Susan Michael
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CHOW, Linda F.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
APPLICANT: PARMLEY, Stephen P.
APPLICANT: REMINGTON, Jack S.
APPLICANT: ARAUJO, Fausto
APPLICANT: SUZUKI, Yashuhiro
APPLICANT: LI, Shuli
TITLE OF INVENTION: ANTIGEN COCKTAIL
FILE REFERENCE: 6361.US.P1
CURRENT APPLICATION NUMBER: US/09/300000
CURRENT FILING DATE: 1999-04-30
EARLIER APPLICATION NUMBER: 09/086,555
EARLIER FILING DATE: 1996-05-28
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Fast SEQ for Windows Version 1.0
SEQ ID NO: 55
LENGTH: 667
TYPE: PRT
ORGANISM: *Toxoplasma gondii*
US-09-303-064-55
Query Match 17.3%; Scored
Best Local Similarity 30.3%; Predicted
Matches 30; Conservative 15; Method M:
GENERAL INFORMATION:
QY 16 QRAAPDVVAFVGPGESQQEERPTDNG
Db 329 QELPPPPTEQBLPPPTPEQELPPTEC
QY 64 QEMDLKURSERGDDGSDVKEKTPPP
Db 389 QQLLEPTE-BEQOBGP-QEPLPPP
RESULT 14
US-09-086-503-55
Sequence 55, Application US/09086503A
Patent No. 6339157
GENERAL INFORMATION:
APPLICANT: MAINE, Gregory T.
APPLICANT: HUNT, Jeffrey C.
APPLICANT: BROJANAC, Susan Michael
APPLICANT: JYH-TSING SHEU, Michael
APPLICANT: CROVAN, Linda E.
APPLICANT: TYNER, Joan D.
APPLICANT: HOWARD, Lawrence V.
TITLE OF INVENTION: ANTIGEN COCKTAIL
FILE REFERENCE: 6361.US.01

```
RESULT 15
US-09-949-016-6170
; Sequence 6170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949
; CURRENT FILING DATE: 2000-04-14
; PRIORITY NUMBER: 60/241,755
; PRIORITY FILING DATE: 2000-10-20
; PRIORITY APPLICATION NUMBER: 60/237,768
; PRIORITY FILING DATE: 2000-10-03
; PRIORITY APPLICATION NUMBER: 60/231,498
; PRIORITY FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO: 6170
; LENGTH: 517
; TYPE: PRO
; ORGANISM: Human
; Us-09-949-016-6170

15; Gaps 4;
Query Match 16.2%; Score 1
Best Local Similarity 29.9%; Pred. 1
Matches 35; Conservative 11; Mismatches 0
QY      9 SGRGGDGAEPWVAFVARGESQQEEF
Db      275 SDGSSSSQEPASKA-KAP--QQEEF
QY      63 -COMMDLEKTRSRGDGSD-
Db      331 TPGEKRKDSSESDSEEDSIDISETA

67;
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KNOWN GENES ASSOCIATED
WITH DISEASES AND METHODS OF DETECTION AND USES THEREOF
016